











Sequences producing significant alignments:

Score E
(bits) Value

gi 39930575 ref NP_937792.1	chromosome 1 open reading fram...	605	e-172	
gi 16306971 gb AAH09553.1	Clorf40 protein [Homo sapiens]	600	e-170	
gi 30424906 ref NP_780468.1	RIKEN cDNA 9330132005 [Mus mus...	553	e-156	
gi 38541263 gb AAH61908.1	Clorf40 protein [Homo sapiens]	551	e-155	
gi 34880246 ref XP_341126.1	similar to scotin [Rattus norv...	550	e-155	
gi 26387842 dbj BAC25627.1	unnamed protein product [Mus mu...	189	8e-47	
gi 27804873 gb AAO22908.1	adventurous gliding motility pro...	60	1e-07	
gi 18418388 ref NP_567956.1	C2 domain-containing protein [...	55	4e-06	
gi 7486289 pir T05421	hypothetical protein F28A23.90 - Ara...	55	4e-06	
gi 41529812 emb CAC86432.1	PGYRP protein [Chlamydomonas re...	54	7e-06	
gi 630791 pir S46965	microfilarial sheath protein - nemato...	53	1e-05	
gi 630789 pir S46964	microfilarial sheath protein - nemato...	52	2e-05	
gi 27682937 ref XP_238028.1	hypothetical protein XP_238028...	52	3e-05	
gi 41054375 ref NP_956004.1	WW domain binding protein 2 [D...	51	6e-05	
gi 22298097 ref NP_681344.1	twitching mobility protein [Th...	51	6e-05	
gi 25446695 gb AAN74842.1	Unknown protein [Oryza sativa (j...	50	8e-05	
gi 4557317 ref NP_001148.1	annexin A11; annexin XI; autoan...	50	8e-05	
gi 20381005 gb AAH28765.1	0610010012Rik protein [Mus muscu...	50	8e-05	
gi 32417300 ref XP_329128.1	predicted protein [Neurospora ...	49	1e-04	
gi 33328913 gb AAQ09863.1	CG16743 [Drosophila yakuba]	49	2e-04	
gi 32411879 ref XP_326420.1	predicted protein [Neurospora ...	49	2e-04	
gi 15228861 ref NP_188919.1	leucine-rich repeat family pro...	49	2e-04	
gi 12963551 ref NP_075657.1	NMDA receptor glutamate-bindin...	49	3e-04	

gi 17568419 ref NP_509224.1 	GrounDhog, hedgehog-like (grd-...	48	3e-04	
gi 37521570 ref NP_924947.1 	unknown protein [Gloeobacter v...	48	5e-04	
gi 30704895 gb AAH51961.1 	2610317D23Rik protein [Mus muscu...	48	5e-04	
gi 15840678 ref NP_335715.1 	hypothetical protein [Mycobact...	47	6e-04	
gi 15608373 ref NP_215749.1 	hypothetical protein Rv1233c [...	47	6e-04	
gi 32489985 emb CAE05015.1 	OSJNBa0044M19.2 [Oryza sativa (...	47	6e-04	
gi 31792426 ref NP_854919.1 	CONSERVED HYPOTHETICAL MEMBRAN...	47	6e-04	
gi 6324205 ref NP_014275.1 	Nuclear Assembly Factor; Naf1p ...	47	8e-04	
gi 40738790 gb EAA57980.1 	hypothetical protein AN6194.2 [A...	46	0.001	
gi 119714 sp P13983 EXTN TOBAC	Extensin precursor (Cell wal...	46	0.001	
gi 15277556 gb AAH12875.1 	Annexin A11 [Mus musculus]	46	0.001	
gi 7304885 ref NP_038497.1 	annexin A11; annexin XI [Mus mu...	46	0.001	
gi 43033512 gb EAB83390.1 	unknown [environmental sequence]	46	0.001	
gi 1002380 gb AAC47514.1 	RRM-type RNA binding protein	46	0.001	
gi 7446344 pir JC5437	spliceosome-associated protein 49 - ...	46	0.001	
gi 34876896 ref XP_237959.2 	similar to annexin A11 [Rattus...	46	0.001	
gi 15235668 ref NP_193070.1 	leucine-rich repeat family pro...	46	0.001	
gi 15021754 gb AAK77904.1 	root nodule extensin [Pisum sati...	46	0.001	
gi 26389968 dbj BAC25820.1 	unnamed protein product [Mus mu...	46	0.001	
gi 38103529 gb EAA50214.1 	hypothetical protein MG03973.4 [...	46	0.001	
gi 15021752 gb AAK77903.1 	root nodule extensin [Pisum sati...	46	0.001	
gi 8132441 gb AAF73291.1 	extensin [Pisum sativum]	46	0.002	
gi 7488765 pir T10863	extensin precursor - kidney bean >gi...	46	0.002	
gi 7441831 pir T06782	extensin - soybean >gi 1165322 gb AA...	45	0.003	
gi 39595249 emb CAE60286.1 	Hypothetical protein CBG03869 [...	45	0.003	
gi 7488673 pir T07622	extensin homolog - soybean (fragment...	45	0.003	
gi 11358038 pir T48627	hypothetical protein T15N1.30 - Ara...	45	0.004	
gi 22530952 gb AAM96980.1 	putative protein [Arabidopsis th...	45	0.004	
gi 42567849 ref NP_196958.2 	proline-rich family protein [A...	45	0.004	
gi 29831993 ref NP_826627.1 	-hypothetical protein [Streptom...	45	0.004	
gi 6912578 ref NP_036522.1 	protein homologous to salivary ...	45	0.004	
gi 20904065 ref XP_139488.1 	similar to hypothetical protei...	45	0.004	
gi 34867281 ref XP_235511.2 	similar to hypothetical protei...	45	0.004	
gi 15610825 ref NP_218206.1 	hypothetical protein Rv3689 [M...	44	0.005	
gi 40741053 gb EAA60243.1 	hypothetical protein AN8694.2 [A...	44	0.005	
gi 31794860 ref NP_857353.1 	PROBABLE CONSERVED TRANSMEMBRA...	44	0.005	
gi 7442095 pir T09965	extensin CYC17 precursor - Madagasca...	44	0.006	
gi 18148443 dbj BAB83257.1 	galectin family xgalectin-IIa [...	44	0.006	
gi 17560702 ref NP_505929.1 	pleckstrin-like (42.2 kD) (5M3...	44	0.006	
gi 119711 sp P06599 EXTN DAUCA	Extensin precursor >gi 82047...	43	0.009	
gi 31455507 dbj EAC77379.1 	putative MAPK activating protei...	43	0.009	
gi 23510333 ref NP_612157.1 	pygopus 2 [Homo sapiens] >gi 2...	43	0.009	
gi 399769 sp Q01493 GP22 LITCA	Major microfilarial sheath p...	43	0.009	
gi 6322645 ref NP_012718.1 	eIF4E-associated protein, binds...	43	0.009	
gi 39595340 emb CAE60377.1 	Hypothetical protein CBG03978 [...	43	0.009	
gi 39593757 emb CAE62050.1 	Hypothetical protein CBG06068 [...	43	0.009	
gi 15021750 gb AAK77902.1 	root nodule extensin [Pisum sati...	43	0.012	
gi 8922157 ref NP_060927.1 	DKFZp564J157 protein [Homo sapi...	43	0.012	
gi 15021742 gb AAK77898.1 	root nodule extensin [Pisum sati...	43	0.012	
gi 2499599 sp Q13164 MK07 HUMAN	Mitogen-activated protein k...	43	0.012	
gi 37681771 gb AAQ97763.1 	cleavage and polyadenylation spe...	43	0.012	
gi 15021748 gb AAK77901.1 	root nodule extensin [Pisum sati...	43	0.012	
gi 12007323 gb AAG45137.1 	unknown [Dictyostelium discoideum]	43	0.012	
gi 24656484 ref NP_611516.1 	CG15225-PA [Drosophila melanog...	43	0.012	
gi 44890757 gb AAH66943.1 	DKFZp564J157 protein [Homo sapiens]	43	0.012	



gi 38175539 dbj EAD01232.1 	proline-rich protein family-lik...	43	0.012	
gi 38303820 gb AAH62074.1 	Grina protein [Rattus norvegicus]	43	0.012	
gi 15021756 gb AAK77905.1 	root nodule extensin [Pisum sati...	43	0.012	
gi 40744469 gb EAA63645.1 	hypothetical protein AN3074.2 [A...	43	0.016	
gi 27803071 emb CAD60774.1 	unnamed protein product [Podosp...	43	0.016	
gi 37532418 ref NP_920511.1 	putative retroelement [Oryza s...	43	0.016	
gi 7271227 emb CAB77678.1 	hypothetical protein L5515.04 [L...	43	0.016	
gi 20376818 ref NP_620431.1 	WW domain binding protein 2 [R...	43	0.016	
gi 12836298 dbj BAB23594.1 	unnamed protein product [Mus mu...	43	0.016	
gi 630627 pir S44809 F44B9.8	protein - Caenorhabditis elegans	43	0.016	
gi 19881654 gb AAM01055.1 	putative pol polyprotein [Oryza ...	43	0.016	
gi 38110299 gb EAA56040.1 	hypothetical protein MG01691.4 [...	43	0.016	
gi 8394539 ref NP_058548.1 	WW domain binding protein 2 [Mu...	43	0.016	
gi 39795834 gb AAH64236.1 	MGC76193 protein [Xenopus tropic...	42	0.021	
gi 33303761 gb AAQ02394.1 	mitogen-activated protein kinase...	42	0.021	
gi 30585137 gb AAP36841.1 	Homo sapiens mitogen-activated p...	42	0.021	
gi 20986501 ref NP_620602.1 	mitogen-activated protein kina...	42	0.021	
gi 20986497 ref NP_002740.2 	mitogen-activated protein kina...	42	0.021	
gi 41055409 ref NP_956928.1 	hypothetical protein MGC63968 ...	42	0.021	
gi 7512757 pir T34520	hypothetical protein DKFZp564J157.1 ...	42	0.021	
gi 20986499 ref NP_620601.1 	mitogen-activated protein kina...	42	0.021	
gi 7018421 emb CAB59179.2 	hypothetical protein [Homo sapiens]	42	0.021	

Alignments

Get selected sequences

Select all

Deselect all

☐ >[gi|39930575|ref|NP_937792.1|](#)  chromosome 1 open reading frame 40 [Homo sapiens]
☒ [gi|37182300|gb|AAQ88952.1|](#)  PPAG583 [Homo sapiens]
 Length = 197

Score = 605 bits (1421), Expect = e-172

Identities = 188/198 (94%), Positives = 188/198 (94%), Gaps = 7/198 (3%)

Query: 1 MPPAGLRW--PLTAIALLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR 58
 MPPAGLR PLTAIALLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR
 Sbjct: 1 MPPAGLRRAAPLTAIALLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR 60

Query: 59 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVA--WATTICCFCLSCCYLYRRRQ 116
 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVA ATTICCFCLSCCYLYRRRQ
 Sbjct: 61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVV-ATTICCFCLSCCYLYRRRQ 119

Query: 117 QLQSPFEGQEIPMTGIPVQPVYPYPQDPM-GPAPPQPGFMYPPSGPAPQYPLYPAGPPVY 175
 QLQSPFEGQEIPMTGIPVQPVYPYPQDPM GPAPPQPGFMYPPSGPAPQYPLYPAGPPVY
 Sbjct: 120 QLQSPFEGQEIPMTGIPVQPVYPYPQDPKAGAPPQPGFMYPPSGPAPQYPLYPAGPPVY 179

Query: 176 NP-MPPPYMPPQPSYPGA 192
 NP PPPYMPPQPSYPGA
 Sbjct: 180 NPAAPPYMPMPQPSYPGA 197

☐ >[gi|16306971|gb|AAH09558.1|](#)  Clorf40 protein [Homo sapiens]

Length = 228

Score = 600 bits (1409), Expect = e-170

Identities = 187/198 (94%), Positives = 188/198 (94%), Gaps = 7/198 (3%)

Query: 1 MPPAGLRW--PLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCGTCYHR 58
 MPPAGLR PLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCGTCYHR
 Sbjct: 32 MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCGTCYHR 91

Query: 59 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVA--WATTICCFLCSCCYLYRRRQ 116
 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVA ATTICCFLCSCCYLYRRRQ
 Sbjct: 92 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVV-ATTICCFLCSCCYLYRRRQ 150

Query: 117 QLQSPFEGQEIPMTGIPVQPVYYPQDPM-GPAPPQPGFMYPPSGPAPQYPLYPAGPPVY 175
 QLQSPFEGQEIPMTGIPVQPVYYPQDP GPAPPQPGF+YPPSGPAPQYPLYPAGPPVY
 Sbjct: 151 QLQSPFEGQEIPMTGIPVQPVYYPQDPKAGAPPQPGFIYPPSGPAPQYPLYPAGPEVY 210

Query: 176 NP-MPPPYMPPQPSYPGA 192
 NP PPPYMPPQPSYPGA
 Sbjct: 211 NPAAPPYMPQPSYPGA 228

>gi|30424906|ref|NP_780468.1| RIKEN cDNA 9330132005 [Mus musculus]
 gi|26333273|dbj|BAC30354.1| unnamed protein product [Mus musculus]
 gi|27924162|gb|AAH44813.1| RIKEN cDNA 9330132005 [Mus musculus]
 Length = 197

Score = 553 bits (1298), Expect = e-156

Identities = 175/199 (87%), Positives = 179/199 (89%), Gaps = 9/199 (4%)

Query: 1 MPPAGLRW---PLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCGTCYH 57
 MPPAG R PL A+ LLVLGAPL LA EDCLWYLDNRNGSWHPGF+CEFFTFCGTCY
 Sbjct: 1 MPPAGPR-GTAPLAAVLLVLGAPLALASEDCCLWYLDNRNGSWHPGFDCEFFTFCGTCYQ 59

Query: 58 RYCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVA--WATTICCFLCSCCYLYRRR 115
 RYCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVA ATTICCFLCSCCYLYRRR
 Sbjct: 60 RYCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVV-ATTICCFLCSCCYLYRRR 118

Query: 116 QQLQSPFEGQEIPMTGIPVQPVYYPQDPM-GPAPPQPGFMYPPSGPAPQYPLYPAGPPV 174
 QQLQS FEGQEIPMTGIP+QPVY YP DP GPAPPQPGFMYPPSGPAPQYPLYPAGPP+
 Sbjct: 119 QQLQSTFEGQEIPMTGIPMQPVYQYPPDPKAGAPPQPGFMYPPSGPAPQYPLYPAGPPI 178

Query: 175 YNP-MPPPYMPPQPSYPGA 192
 YNP PPPYMPPQPSYPGA
 Sbjct: 179 YNPAAAPPYMPQPSYPGA 197

>gi|38541263|gb|AAH61908.1| Clorf40 protein [Homo sapiens]
 Length = 176

Score = 551 bits (1292), Expect = e-155

Identities = 169/177 (95%), Positives = 170/177 (96%), Gaps = 5/177 (2%)

Query: 20 APLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCGTCYHRYCCRDLTLLITERQQKHCLAF 79
 APLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCGTCYHRYCCRDLTLLITERQQKHCLAF
 Sbjct: 1 APLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCGTCYHRYCCRDLTLLITERQQKHCLAF 60

Query: 80 SPKTIAGIASAVILFVA--WATTICCFLCSCCYLYRRRQQLQSPFEGQEIPMTGIPVQPV 137
 SPKTIAGIASAVILFVA ATTICCFLCSCCYLYRRRQQLQSPFEGQEIPMTGIPVQPV
 Sbjct: 61 SPKTIAGIASAVILFVAVV-ATTICCFLCSCCYLYRRRQQLQSPFEGQEIPMTGIPVQPV 119

Query: 138 YPYPQDPM-GPAPPQPGFMYPPSGPAPQYPLYAGPPVYNP-MPPPYMPPQPSYPGA 192
 YPYPQDP GPAPPQPGF+YPPSGPAPQYPLYAGPPVYNP PPPYMPQPSYPGA
 Sbjct: 120 YPYPQDPKAGPAPPQPGFIYPPSGPAPQYPLYAGPPVYNPAAPPPYMPQPSYPGA 176

>gi|34880246|ref|XP_341126.1| similar to scotin [Rattus norvegicus]
 Length = 197

Score = 550 bits (1290), Expect = e-155
 Identities = 174/199 (87%), Positives = 178/199 (89%), Gaps = 9/199 (4%)

Query: 1 MPPAGLRW---PLTAIALLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTCCGTCYH 57
 MPPAG R PL A+ LLVLGAPL LA EDCLWYLDNRNGSWHPGF+CEFFTCCGTCY
 Sbjct: 1 MPPAGPR-GVAPLAADVLLVLGAPLALASEDCWYLDNRNGSWHPGFDCEFFTCCGTCYQ 59

Query: 58 RYCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVA--WATTICCFLCSCCYLYRRR 115
 RYCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVA ATTICCFLCSCCYLYRRR
 Sbjct: 60 RYCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVV-ATTICCFLCSCCYLYRRR 118

Query: 116 QQLQSPFEGQEIPMTGIPVQPVYYPQDPM-GPAPPQPGFMYPPSGPAPQYPLYAGPPV 174
 QQLQS FEGQEIPMTGIP+QPVY YP DP GP PPQPGFMYPPSGPAPQYPLYAGPP+
 Sbjct: 119 QQLQSTFEGQEIPMTGIPMQPVYQYPPDPKAGPGPPQPGFMYPPSGPAPQYPLYAGPPI 178

Query: 175 YNP-MPPPYMPPQPSYPGA 192
 YNP PPPYMPQPSYPGA
 Sbjct: 179 YNPAAAPPPYMPQPSYPGA 197

>gi|26387842|dbj|BAC25627.1| unnamed protein product [Mus musculus]
 Length = 146

Score = 189 bits (440), Expect = 8e-47
 Identities = 53/56 (94%), Positives = 54/56 (96%)

Query: 24 LAGEDCLWYLDNRNGSWHPGFNCEFFTCCGTCYHRYCCRDLTLLITERQQKHCLAF 79
 LA EDCLWYLDNRNGSWHPGF+CEFFTCCGTCY RYCCRDLTLLITERQQKHCLAF
 Sbjct: 66 LASEDCWYLDNRNGSWHPGFDCEFFTCCGTCYQRYCCRDLTLLITERQQKHCLAF 121

>gi|27804873|gb|AAO22908.1| adventurous gliding motility protein X [Myxococcus x]
 Length = 674

Score = 59.6 bits (133), Expect = 1e-07
 Identities = 33/78 (42%), Positives = 35/78 (44%), Gaps = 34/78 (43%)

Query: 124 GQEIPMTGIPVQPVY---PYPQDPMG----PAP-P---QPGFMYPPSGPAPQYPLYAGP 172
 G E+PM QP+ PY Q PM PAP P QPG PQY
 Sbjct: 316 GAEVPMA----QPMASPMYPGQQPMQQYPQFAPMPYGHQPG-----PQYA----- 356

Query: 173 PVYNPMPPPYMPPQPSYP 190
 PMP PY PPQPSYP
 Sbjct: 357 ---QPMAPY-PPQPSYP 370

>[gi|18418388|ref|NP_567956.1|](#) C2 domain-containing protein [Arabidopsis thaliana]
[gi|15724316|gb|AAL06551.1|](#) AT4g34150/F28A23_90 [Arabidopsis thaliana]
[gi|23397247|gb|AAN31905.1|](#) unknown protein [Arabidopsis thaliana]
 Length = 247

Score = 54.5 bits (121), Expect = 4e-06
 Identities = 35/71 (49%), Positives = 35/71 (49%), Gaps = 29/71 (40%)

Query: 138 YP----YPQDPMG--PA---PPQPGFMYP--SGPAPQYP----LYPAGPP--VYNPMP 179
 YP YPQ P G PA PPQP YPP SG YP YP PP Y P
 Sbjct: 172 YPQVQQYPQ-PSGYPPASGYPPQPS-AYPPPSTSG----YPPIPSAYPPPPSSAY---P 222

Query: 180 P-PYMPPQPSY 189
 P PY PPQPSY
 Sbjct: 223 PQPY-PPQPSY 232

>[gi|7486289|pir||T05421](#) hypothetical protein F28A23.90 - Arabidopsis thaliana
[gi|2911047|emb|CAA17557.1|](#) putative protein [Arabidopsis thaliana]
[gi|7270364|emb|CAB80132.1|](#) putative protein [Arabidopsis thaliana]
 Length = 279

Score = 54.5 bits (121), Expect = 4e-06
 Identities = 35/71 (49%), Positives = 35/71 (49%), Gaps = 29/71 (40%)

Query: 138 YP----YPQDPMG--PA---PPQPGFMYP--SGPAPQYP----LYPAGPP--VYNPMP 179
 YP YPQ P G PA PPQP YPP SG YP YP PP Y P
 Sbjct: 191 YPQVQQYPQ-PSGYPPASGYPPQPS-AYPPPSTSG----YPPIPSAYPPPPSSAY---P 241

Query: 180 P-PYMPPQPSY 189
 P PY PPQPSY
 Sbjct: 242 PQPY-PPQPSY 251

>[gi|41529812|emb|CAC86432.1|](#) PGYRP protein [Chlamydomonas reinhardtii]
[gi|41529814|emb|CAD32174.1|](#) proline-glycine-tyrosine rich protein [Chlamydomonas]
 Length = 169

Score = 53.7 bits (119), Expect = 7e-06
 Identities = 36/77 (46%), Positives = 37/77 (48%), Gaps = 32/77 (41%)

Query: 136 PVYP--YPQDPMGPA--PPQPGFMYP-PSG--PAPQYPL---YPAGP-----PVYNPMP 180
 P YP YP P PA PPQP YP P+G P P YP YP P P Y PP
 Sbjct: 12 PGYPPGY--P--PAGYPPQPG--YPAPAGYPPQPGYPPQPGYPPQPGYPPQPGY---PP 62

Query: 181 P-----YMPPQPSYP 190
 P Y PPQP YP
 Sbjct: 63 PAGYPAPGY-PPQPGYP 78


>[gi|630791|pir||S46965](#) microfilarial sheath protein - nematode (Brugia pahangi)
[gi|516355|emb|CAA84597.1|](#) microfilarial sheath protein [Brugia pahangi]
 Length = 228

Score = 53.2 bits (118), Expect = 1e-05
 Identities = 35/78 (44%), Positives = 36/78 (46%), Gaps = 26/78 (33%)

Query: 128 PMTGIPVQPVYP----YPQDPMGPAPPQPGFMYPPSGPAPQYPL---YPAGPPVYNPMPP 180
 PM +P P YP YPQ P P PPQ YP APQYP YP P Y P PP
 Sbjct: 120 PM--VPQPPQYPQPPQYPQPPQYPQPPQ----YPQ---APQYPQAPQYPQVPQ-Y-PQPP 168
 Query: 181 PYMPPQ-----PSYP 190
 Y PPQ P YP
 Sbjct: 169 QYQPPQYQPPQYQPPQYP 186



Score = 29.5 bits (62), Expect = 141
 Identities = 21/53 (39%), Positives = 22/53 (41%), Gaps = 27/53 (50%)

Query: 136 PVYP---YPQDPMGPA-----PPQPGFMYPPSGP----APQYPLYP-AG 171
 P YP YPQ P PPQ Y P P AP+YP YP AG
 Sbjct: 156 PQYPQVPQYPQ---PPQYQPPQYQPPQ---YQP--PQYPKAPKYPOYPTAG 198

 >[gi|630789|pir||S46964](#) microfilarial sheath protein - nematode (Brugia malayi)
[gi|516353|emb|CAA84596.1|](#) microfilarial sheath protein [Brugia malayi]
 Length = 237

Score = 52.0 bits (115), Expect = 2e-05
 Identities = 35/84 (41%), Positives = 36/84 (42%), Gaps = 31/84 (36%)

Query: 128 PMTGIPVQPVYP-----YPQDPMGPAPPQPGFMYPPSGPAPQYPL---YPAGP-- 172
 PM +P P YP YPQ P P PQ YP APQYP YP P
 Sbjct: 121 PM--VPQPPQYPQLPQYTQPPQYPQAPQYPQAPQ---YPQ---APQYPQAPQYPQAPQY 171
 Query: 173 ---PVYNPMPPPYMPPQ---PSYP 190
 P Y P PP Y PPQ P YP
 Sbjct: 172 PQVPQY-PQPPQYQPPQYQPPQYP 194

 >[gi|27682937|ref|XP_238028.1|](#)  hypothetical protein XP_238028 [Rattus norvegicus]
 Length = 103

Score = 51.5 bits (114), Expect = 3e-05
 Identities = 25/53 (47%), Positives = 26/53 (49%), Gaps = 20/53 (37%)

Query: 139 PYPQDPMGP--APPQPGFMYPPSGPAPQ-----YPLY-----PAGPP---VY 175
 PYPQ PMGP APP G+ YPP PQ YP Y P PP VY
 Sbjct: 20 PYPQQPMGPMGAPPQGYPYPP---PQGYPYQGYPGWQGGPQEPPKTTVY 68

Score = 38.8 bits (84), Expect = 0.22
 Identities = 24/52 (46%), Positives = 25/52 (48%), Gaps = 12/52 (23%)

Query: 145 MGPAPPQPGFMYPPSGPAPQYPLYYPAGPPVYNPM--PP----PYMPPQPSYP 190
 M P P P YP GP YP YP P+ PM PP PY PPQ YP
 Sbjct: 1 MNPENPPP---YPGPGPTAPYPYPYQ-QPM-GPMGAPPQGYPYPPPQ-GYP 46

>[gi|41054375|ref|NP_956004.1|](#) WW domain binding protein 2 [Danio rerio]
[gi|31419213|gb|AAH53232.1|](#) WW domain binding protein 2 [Danio rerio]
 Length = 255

Score = 50.7 bits (112), Expect = 6e-05
 Identities = 30/51 (58%), Positives = 30/51 (58%), Gaps = 13/51 (25%)

Query: 147 PAPPQPGFMYP-PSGP-AP--QYPLY-PA-GPPVYNMPPPPYMPPQPSYPG 191
 PA PQP YP PS P AP QYP Y PA G VY P P YM P P YPG
 Sbjct: 157 PAMPQP--YPYPSMPQAPYSQYP-YAPAAG--VY-PSAPVYMAPPPPYPG 200

Score = 41.8 bits (91), Expect = 0.028
 Identities = 34/97 (35%), Positives = 35/97 (36%), Gaps = 54/97 (55%)

Query: 135 QPVYYPQDPMGPAP-PQPGFMYP-----PSGP--APQYPLYPAGPP-----V- 174
 QP YPYP M AP Q YP PS P AP P YP GPP V
 Sbjct: 161 QP-YPYP--SMPQAPYSQ----YPYAPAAGVYPSAPVYMAPP-PPYP-GPPQDWAALPVA 211

Query: 175 -----YNP-----MP----PPYMPPQ 186
 YNP MP PPY PP+
 Sbjct: 212 PANAKAAEAASSAFYNPSNPHSVYMPSDLPPPYFPPE 248

>[gi|22298097|ref|NP_681344.1|](#) twitching mobility protein [Thermosynechococcus el
[gi|22294275|dbj|BAC08106.1|](#) twitching mobility protein [Thermosynechococcus elong
 Length = 446

Score = 50.7 bits (112), Expect = 6e-05
 Identities = 30/56 (53%), Positives = 30/56 (53%), Gaps = 19/56 (33%)

Query: 144 PMGPA---PPQPFGMYPPSGPAPQYPLYPAG-PPVYNMPP-----PYMPPQP 187
 PMG A PPQPG M PP PAP P P G PP PMPP P MPPQP
 Sbjct: 25 PMGAAVPPMPPQPG-MAPPR-PAPPPP--PQGMPP--RPMPPQPGMPPRP-MPPQP 73

>[gi|25446695|gb|AAN74842.1|](#) Unknown protein [Oryza sativa (japónica cultivar-gro
 Length = 241


Score = 50.3 bits (111), Expect = 8e-05
 Identities = 34/72 (47%), Positives = 35/72 (48%), Gaps = 29/72 (40%)


Query: 133 PVQPVY--PY---PQDPMGPAPPQPGFMYPSPG--PA--PQ---YPLYPAGPPVYNMPP 180
 P QP Y PY P PAPP G YPP+ PA PQ YP P G Y PP
 Sbjct: 177 PQQPAYGQPYGGYP-----PAPPAQG--YPPAAYPPAGYPQGGAYP--PPGS--Y---PP 222


Query: 181 P--YMPPQPSYP 190
 P Y PPQ SYP
 Sbjct: 223 PGSY-PPQGSYP 233

>[gi|4557317|ref|NP_001148.1|](#) annexin A11; annexin XI; autoantigen, 56-kD; calc


annexin 50 [Homo sapiens]

[gi|22165431|ref|NP_665875.1|](#)  annexin A11; annexin XI; autoantigen, 56-kD; calcy
annexin 50 [Homo sapiens]

[gi|22165433|ref|NP_665876.1|](#)  annexin A11; annexin XI; autoantigen, 56-kD; calcy
annexin 50 [Homo sapiens]

[gi|1703322|sp|P50995|ANXB_HUMAN](#)  Annexin A11 (Annexin XI) (Calcyclin-associated
(56 kDa autoantigen)

[gi|1082212|pir||A53152](#) annexin XI - human

[gi|457129|gb|AA19734.1|](#)  56K autoantigen

[gi|8671171|emb|CAB94995.1|](#)  annexin A11 [Homo sapiens]

[gi|8671173|emb|CAB94996.1|](#)  annexin A11 [Homo sapiens]

[gi|8671175|emb|CAB94997.1|](#)  annexin A11 [Homo sapiens]

[gi|14043153|gb|AAH07564.1|](#)  Annexin A11 [Homo sapiens]

Length = 505

Score = 50.3 bits (111), Expect = 8e-05

Identities = 36/91 (39%), Positives = 38/91 (41%), Gaps = 47/91 (51%)


Query: 138 YP-----YPQDPMGPAPP-----QP----GFMYPSPG---PA--PQYPLYPAGP 172
YP YP P PP QP G MYPP G P+ P YP YP G
Sbjct: 74 YPGAPGAGYP----PVPPGGFGQPPSAQQVPVPYGY-MYPPPGGNPPSRMPSPYPPYP-GA 126

Query: 173 PVYNP---MPPP-----YMPPQP--SYPG 191
PV P MPPP Y P QP +YPG
Sbjct: 127 PV--PGQPMPPPGQQPPGAY-PGQPPVTPY 154

Score = 30.3 bits (64), Expect = 79

Identities = 21/52 (40%), Positives = 22/52 (42%), Gaps = 22/52 (42%)

Query: 138 YP-YPQDPMGPAPPQPGFMYPPSGPAPQYPLYPAGP---PVYNPMPPPYMPP 185
YP YP PP G YPP+ P GP Y P PPP MPP
Sbjct: 3 YPGYP-----PPPGG--YPPAAPG-----GGPWGGAAY-P-PPPSMPP 36

[gi|20381005|gb|AAH28765.1|](#)  0610010012Rik protein [Mus musculus]
Length = 104

Score = 50.3 bits (111), Expect = 8e-05

Identities = 25/56 (44%), Positives = 26/56 (46%), Gaps = 23/56 (41%)

Query: 139 PYPQDPMGP-----APPQPGFMYPPSGPAPQ-----YPLY-----PAGPP---VY 175
PYPQ PMGP APP G+ YPP PQ YP Y P PP VY
Sbjct: 20 PYPQQPMGPMGPMGAPPPQGYPPYPP---PQGYPYQGYPQYGWQGGPQEPPKTTVY 71

Score = 40.1 bits (87), Expect = 0.091

Identities = 25/54 (46%), Positives = 26/54 (48%), Gaps = 13/54 (24%)

Query: 145 MGPAPPQPGFMYPPSGPAPQYPLYPAGP--PVYNPM--PP----PYMPPQPSYP 190
M P P P YP GP YP YP P P+ PM PP PY PPQ YP
Sbjct: 1 MNPENPPP---YPGPGTAPYPPYPQQPMGPM-GPMGAPPPQGYPPPPQ-GYP 49